

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> RuvB Polynucleotides and Uses Thereof

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<150> US 60/144,112

<151> 1999-07-16

<150> US 09/589,510

<151> 2000-06-07

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Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly
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ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc gtg ggc      207
Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe Val Gly
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cag tcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg att cgc      255
Gln Ser Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg
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cag aaa aag atg gcc ggc cgc gcg gtg ctc ctt gtg ggt ccg ccc gcc      303
Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Val Gly Pro Pro Ala
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acg ggc aag acg gcg cta gcg ctc ggc ata gcc cag gag ctc ggc agc      351
Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser
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aag gtc cct ttc tgc cct atg gta gga tca gaa gtg tac tcc tcg gag      399

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gtg ggc cag gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg      258
Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met
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att cgc cag aag aag atg gcc ggc cgc gcg gtg ctc ctt gcg ggt ccg      306
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ata ggt ttg cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt      498
Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val
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act gaa ctt tcc cca gaa gag gct gag agt aca act ggt gga tat gca      546
Thr Glu Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala
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aaa agc att agc cat gta atc atc agc tta aag act gtt aaa ggg act      594
Lys Ser Ile Ser His Val Ile Ile Ser Leu Lys Thr Val Lys Gly Thr
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aag caa ctg aag tta gat tct tca att tat gat gct ctg atc aag gaa      642
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 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
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 Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser
 145 150 155 160
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 Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr
 180 185 190
 Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
 195 200 205
 Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro
 210 215 220
 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu
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His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
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 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
 260 265 270
 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
 275 280 285
 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
 290 295 300
 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
 305 310 315 320
 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
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 Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp
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 Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp
 370 375 380
 Met Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr
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 Ser Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser
 405 410 415
 Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val
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 Met Arg Ile Glu Glu Val Gln Ser Thr Ser
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 aag aag cag cgc atc gcc acc cac act cac atc aag ggc ctc ggc ctc 159
 Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly Leu 25
 15 20
 gac gcc aat gga atg tcg atg ccg ttg gcg gcg ggg ttc gtg ggc cag 207
 Asp Ala Asn Gly Met Ser Met Pro Leu Ala Ala Gly Phe Val Gly Gln 40
 30 35 40
 gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg atc cgc cag 255
 Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg Gln 55
 45 50 55

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ggc aaa acg gcg cta gcg ctc ggc ata gcg cag gag ctc ggc agc aag Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys 75 80 85 90	351
gtc cca ttc tgt cct atg gta gga tca gaa gtg tac tcc tca gag gtc Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu Val 95 100 105	399
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cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt att gaa ctt Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val Ile Glu Leu 125 130 135	495
tcc cca gaa gag gct gag agc aca act ggt gga tat gcg aaa agc att Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile 140 145 150	543
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caa ggt ggc caa gat att ttg tcc ctt atg ggc cag atg atg aag cca Gln Gly Gly Gln Asp Ile Leu Ser Leu Met Gly Gln Met Met Lys Pro 255 260 265	879
cgg aag act gaa atc acc gaa aag cta cgc caa gaa atc aat aag gtg Arg Lys Thr Glu Ile Thr Glu Lys Leu Arg Gln Glu Ile Asn Lys Val 270 275 280	927

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Val Asn Arg Tyr Ile Asp Glu Gly Ile Ala Glu Leu Val Pro Gly Val	
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Leu Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Tyr	
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Leu Asn Arg Ala Leu Glu Ser Pro Leu Ser Pro Ile Val Ile Leu Ala	
315 320 325 330	
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Thr Asn Arg Gly Ile Cys Asn Val Arg Gly Thr Asp Met Thr Ser Pro	
335 340 345	
cat ggt ata cca gtg gac ctt cta gat agg ttg gtg att att cgg aca	1167
His Gly Ile Pro Val Asp Leu Leu Asp Arg Leu Val Ile Ile Arg Thr	
350 355 360	
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Glu Thr Tyr Gly Pro Thr Glu Met Ile Gln Ile Leu Ala Ile Arg Ala	
365 370 375	
caa gtg gaa gag att gat atc gat gaa gaa agt ctt gct tat tta ggc	1263
Gln Val Glu Glu Ile Asp Ile Asp Glu Glu Ser Leu Ala Tyr Leu Gly	
380 385 390	
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Glu Ile Gly Gln Gln Thr Ser Leu Arg His Ala Ile Gln Leu Leu Ser	
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cct gcc agc gtg gtc gca aag acc aac ggg aga gaa aag atg tgc aag	1359
Pro Ala Ser Val Val Ala Lys Thr Asn Gly Arg Glu Lys Met Cys Lys	
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Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser	
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gct cgc ctg ctc cag gag caa caa gaa aga tac atc acc tagacttgca	1456
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<213> Zea mays

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Val	Gly	Ser	Glu	Val	Tyr	Ser	Ser	Glu	Val	Lys	Lys	Thr	Glu	Val	Leu	
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Glu	Val	Tyr	Glu	Gly	Glu	Val	Ile	Glu	Leu	Ser	Pro	Glu	Glu	Ala	Glu	
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Ser	Thr	Thr	Gly	Gly	Tyr	Ala	Lys	Ser	Ile	Ser	His	Val	Ile	Ile	Gly	
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Tyr	Asp	Ala	Leu	Ile	Lys	Glu	Lys	Val	Ala	Val	Gly	Asp	Val	Ile	Tyr	
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Ile	Glu	Ala	Asn	Ser	Gly	Ala	Val	Lys	Arg	Val	Gly	Arg	Cys	Asp	Ser	
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Phe	Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	Glu	Glu	Tyr	Val	Pro	Ile	Pro	
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Lys	Gly	Glu	Val	His	Lys	Lys	Lys	Glu	Ile	Val	Gln	Asp	Val	Thr	Leu	
225					230					235					240	
His	Asp	Leu	Asp	Ala	Ala	Asn	Ala	Gln	Pro	Gln	Gly	Gly	Gln	Asp	Ile	
				245					250					255		
Leu	Ser	Leu	Met	Gly	Gln	Met	Met	Lys	Pro	Arg	Lys	Thr	Glu	Ile	Thr	
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Glu	Lys	Leu	Arg	Gln	Glu	Ile	Asn	Lys	Val	Val	Asn	Arg	Tyr	Ile	Asp	
		275					280					285				
Glu	Gly	Ile	Ala	Glu	Leu	Val	Pro	Gly	Val	Leu	Phe	Ile	Asp	Glu	Val	
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His	Met	Leu	Asp	Ile	Glu	Cys	Phe	Ser	Tyr	Leu	Asn	Arg	Ala	Leu	Glu	
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Ser	Pro	Leu	Ser	Pro	Ile	Val	Ile	Leu	Ala	Thr	Asn	Arg	Gly	Ile	Cys	
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Asn	Val	Arg	Gly	Thr	Asp	Met	Thr	Ser	Pro	His	Gly	Ile	Pro	Val	Asp	
		340						345					350			
Leu	Leu	Asp	Arg	Leu	Val	Ile	Ile	Arg	Thr	Glu	Thr	Tyr	Gly	Pro	Thr	
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Glu	Met	Ile	Gln	Ile	Leu	Ala	Ile	Arg	Ala	Gln	Val	Glu	Glu	Ile	Asp	
	370					375					380					
Ile	Asp	Glu	Glu	Ser	Leu	Ala	Tyr	Leu	Gly	Glu	Ile	Gly	Gln	Gln	Thr	
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Ser	Leu	Arg	His	Ala	Ile	Gln	Leu	Leu	Ser	Pro	Ala	Ser	Val	Val	Ala	
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ttg atc aag gaa aag gtg gca gtg ggt gat gtt ata tac att gaa gca Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr Ile Glu Ala 185 190 195			753
aat agt gga gca gtg aaa aga gtt ggt aga tgt gat tct ttt gct aca Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser Phe Ala Thr 200 205 210			801
gaa tat gat ctt gaa gct gaa gag tat gtt cct atc ccc aaa ggt gaa Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro Lys Gly Glu 215 220 225			849
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gat gca gca aat gcc cag cca caa ggt ggc caa gat att ttg tcc ctt Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile Leu Ser Leu 245 250 255 260			945
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cgc caa gaa atc aat aag gtg gta aac aga tat atc gac gaa gga atc Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp Glu Gly Ile 280 285 290			1041
gca gag ctt gta cct ggt gtt ttg ttc att gat gag gtc cac atg ttg Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val His Met Leu 295 300 305			1089
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tca cca att gtg ata ctc gct acg aat aga gga ata tgt aat gtg aga Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys Asn Val Arg 325 330 335 340			1185
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360	365	370	
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Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp Ile Asp Glu			
375	380	385	
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Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser Leu Arg			
390	395	400	
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His Ala Ile Gln Leu Leu Ser Pro Ala Ser Val Val Ala Lys Thr Asn			
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Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln Gln Glu			
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aga tac atc acc tagacttgca tctcctgctg tggaaggaaa agcctcgaag			1573
Arg Tyr Ile Thr			
455			
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Ala Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly			
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Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile				
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Gly Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Pro Ser				160
	165		170	175
Ile Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile				
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Tyr Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp				
	195		200	205
Ser Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile				
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Pro Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr				240
225		230		235
Leu His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp				255
	245		250	255
Ile Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile				
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Thr Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile				
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Asp Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu				
	290		295	300
Val His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu				320
305		310		315
Glu Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile				335
	325		330	335
Cys Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val				
	340		345	350
Asp Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro				
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Thr Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile				
	370		375	380
Asp Ile Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln				400
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Thr Ser Leu Arg His Ala Ile Gln Leu Leu Ser Pro Ala Ser Val Val				415
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Ala Lys Thr Asn Gly Arg Glu Lys Met Cys Lys Ala Asp Leu Glu Glu				
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Met Arg Ile Glu Glu Val Gln Ser Thr Ser Lys Lys Gln Arg Ile

1

5

10

15

60

108

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gcg ggc ata gcc cag gag ctc ggc agc aag gtc cct ttc tgt cct atg Ala Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met 65 70 75	300
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tct ttg aga cat gct att caa ttg ata tca cct gcc agc gtg gtc tca Ser Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser 385 390 395	1260
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<400> 10

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Ile	Ala	Leu	Ala	Ala	Gly	Phe	Val	Gly	Gln	Lys	Lys	Met	Ala	Gly	Arg	40	45	50	55
Ala	Val	Leu	Leu	Ala	Gly	Pro	Pro	Ala	Thr	Gly	Lys	Thr	Ala	Leu	Ala	60	65	70	75
Gly	Ile	Ala	Gln	Glu	Leu	Gly	Ser	Lys	Val	Pro	Phe	Cys	Pro	Met	Val	80	85	90	95
Gly	Ser	Glu	Val	Tyr	Ser	Ser	Glu	Val	Lys	Lys	Thr	Glu	Val	Leu	Met	100	105	110	115
Glu	Asn	Phe	Arg	Arg	Ala	Ile	Gly	Leu	Arg	Ile	Lys	Glu	Asn	Lys	Glu	120	125	130	135
Val	Tyr	Glu	Gly	Glu	Val	Thr	Glu	Leu	Ser	Pro	Glu	Glu	Ala	Glu	Ser	140	145	150	155
Thr	Thr	Gly	Gly	Tyr	Ala	Lys	Ser	Ile	Ser	His	Val	Ile	Ile	Ser	Leu	160	165	170	175
Lys	Thr	Val	Lys	Gly	Thr	Lys	Gln	Leu	Lys	Leu	Asp	Ser	Ser	Ile	Tyr	180	185	190	195
Asp	Ala	Leu	Ile	Lys	Glu	Lys	Val	Ala	Val	Gly	Asp	Val	Ile	Tyr	Ile	200	205	210	215
Glu	Ala	Asn	Ser	Gly	Ala	Val	Lys	Arg	Val	Gly	Arg	Cys	Asp	Ser	Phe	220	225	230	235
Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	Glu	Glu	Tyr	Val	Pro	Ile	Pro	Lys	240	245	250	255
Gly	Glu	Val	His	Lys	Lys	Lys	Glu	Ile	Val	Gln	Asp	Val	Thr	Leu	His	260	265	270	275
Asp	Leu	Asp	Ala	Ala	Asn	Ala	Gln	Pro	Gln	Gly	Gly	Gln	Asp	Ile	Leu	280	285	290	295
Ser	Leu	Met	Gly	Gln	Met	Met	Lys	Pro	Arg	Lys	Thr	Glu	Ile	Thr	Glu	300	305	310	315
Lys	Leu	Arg	Gln	Glu	Ile	Asn	Lys	Val	Val	Asn	Arg	Tyr	Ile	Asp	Glu	320	325	330	335
Gly	Ile	Ala	Glu	Leu	Val	Pro	Gly	Val	Leu	Phe	Ile	Asp	Glu	Val	His	340	345	350	

Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Glu Ile Asp Met
 355 360 365
 Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr Ser
 370 375 380
 Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser Lys
 385 390 395 400
 Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val Ser
 405 410 415
 Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu Gln
 420 425 430
 Gln Glu Arg Tyr Ile Thr
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<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

<400> 11

tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa

36